

- 80 -

SEQUENCE LISTING

<110> Acton, Susan

5 <120> NOVEL PROTEIN KINASE MOLECULES AND USES THEREFOR

<130> MNI-050

<140>

10 <141>

<160> 15

<170> PatentIn Ver. 2.0

15

<210> 1

<211> 4137

<212> DNA

<213> Homo sapiens

20

<220>

<221> CDS

<222> (297) .. (1202)

25 <400> 1

tcgacccacg cgctccgggag gatcgggagt cgcgggagga tgggccgccg ctaggctcgc 60

actccggacg cgctcgcag tgccgagggt gggcgccccg cgctgcagc gtccgccggg 120

30 gcggcgccggc gggaggtggc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180

cgcgctttcc gacggcggcg ccgcgcgcag ccacccgcc gcccaaggtc tctcgccggc 240

35 gggagaacgg aaaactccca acttctcgag ttctaaagtt cctgttgctt cagaca atg 299
Met

1

gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347

40 Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln
5 10 15

cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395

Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn
20 25 30

45

ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443

Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr
35 40 45

50 aga gca gcc tgt ctg ttg gat gga gta cca gta gct tta aaa aaa gtg 491

Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val
50 55 60 65

cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539

- 81 -

	Gln	Ile	Phe	Asp	Leu	Met	Asp	Ala	Lys	Ala	Arg	Ala	Asp	Cys	Ile	Lys	
					70					75					80		
5	gaa	ata	gat	ctt	ctt	aag	caa	ctc	aac	cat	cca	aat	gta	ata	aaa	tat	587
	Glu	Ile	Asp	Leu	Leu	Lys	Gln	Leu	Asn	His	Pro	Asn	Val	Ile	Lys	Tyr	
				85					90					95			
10	tat	gca	tca	ttc	att	gaa	gat	aat	gaa	cta	aac	ata	gtt	ttg	gaa	cta	635
	Tyr	Ala	Ser	Phe	Ile	Glu	Asp	Asn	Glu	Leu	Asn	Ile	Val	Leu	Glu	Leu	
			100					105					110				
15	gca	gat	gct	ggc	gac	cta	tcc	aga	atg	atc	aag	cat	ttt	aag	aag	caa	683
	Ala	Asp	Ala	Gly	Asp	Leu	Ser	Arg	Met	Ile	Lys	His	Phe	Lys	Lys	Gln	
			115				120					125					
20	aag	agg	cta	att	cct	gaa	aga	act	gtt	tgg	aag	tat	ttt	gtt	cag	ctt	731
	Lys	Arg	Leu	Ile	Pro	Glu	Arg	Thr	Val	Trp	Lys	Tyr	Phe	Val	Gln	Leu	
			130			135				140					145		
25	tgc	agt	gca	ttg	gaa	cac	atg	cat	tct	cga	aga	gtc	atg	cat	aga	gat	779
	Cys	Ser	Ala	Leu	Glu	His	Met	His	Ser	Arg	Arg	Val	Met	His	Arg	Asp	
					150					155					160		
30	ata	aaa	cca	gct	aat	gtg	ttc	att	aca	gcc	act	ggg	gtg	gta	aaa	ctt	827
	Ile	Lys	Pro	Ala	Asn	Val	Phe	Ile	Thr	Ala	Thr	Gly	Val	Val	Lys	Leu	
				165					170				175				
35	gga	gat	ctt	ggg	ctt	ggc	cgg	ttt	ttc	agc	tca	aaa	acc	aca	gct	gca	875
	Gly	Asp	Leu	Gly	Leu	Gly	Arg	Phe	Phe	Ser	Ser	Lys	Thr	Thr	Ala	Ala	
			180				185						190				
40	cat	tct	tta	gtt	ggt	acg	cct	tat	tac	atg	tct	cca	gag	aga	ata	cat	923
	His	Ser	Leu	Val	Gly	Thr	Pro	Tyr	Tyr	Met	Ser	Pro	Glu	Arg	Ile	His	
			195				200					205					
45	gaa	aat	gga	tac	aac	ttc	aaa	tct	gac	atc	tgg	tct	ctt	ggc	tgt	cta	971
	Glu	Asn	Gly	Tyr	Asn	Phe	Lys	Ser	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Leu	
			210			215				220					225		
50	cta	tat	gag	atg	gct	gca	tta	caa	agt	cct	ttc	tat	ggt	gac	aaa	atg	1019
	Leu	Tyr	Glu	Met	Ala	Ala	Leu	Gln	Ser	Pro	Phe	Tyr	Gly	Asp	Lys	Met	
				230						235					240		
55	aat	tta	tac	tca	ctg	tgt	aag	aag	ata	gaa	cag	tgt	gac	tac	cca	cct	1067
	Asn	Leu	Tyr	Ser	Leu	Cys	Lys	Lys	Ile	Glu	Gln	Cys	Asp	Tyr	Pro	Pro	
				245					250					255			
60	ctt	cct	tca	gat	cac	tat	tca	gaa	gaa	ctc	cga	cag	tta	gtt	aat	atg	1115
	Leu	Pro	Ser	Asp	His	Tyr	Ser	Glu	Glu	Leu	Arg	Gln	Leu	Val	Asn	Met	
			260					265					270				
65	tgc	atc	aac	cca	gat	cca	gag	aag	cga	cca	gac	gtc	acc	tat	gtt	tat	1163
	Cys	Ile	Asn	Pro	Asp	Pro	Glu	Lys	Arg	Pro	Asp	Val	Thr	Tyr	Val	Tyr	
			275				280					285					

- 82 -

gac gta gca aag agg atg cat gca tgc act gca agc agc taaacatgca 1212
 Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
 290 295 300

5 agatcatgaa gagtgtaacc aaagtaattg aaagtatttt gtgcaaagtc gtacctsccc 1272
 atttatgtct ggggtgtaag attaataattt cagagctagt gtgctctgaa tccttaacca 1332
 10 gttttcatat aagcttcatt ttgtaccagt cacctaaatc acctccttgc aacccccaaa 1392
 tgactttgga ataactgaat tgcattgttag gagagaaaat gaaacatgat ggttttgaat 1452
 ggctaaaggt ttatagaatt tcttacagtt ttctgctgat aaattgtgtt tagatagact 1512
 15 gtcagtgcc aatattgaag gtgcagcttg gcacacatca gaatagactc atacctgaga 1572
 aaaagtatct gaacatgtga cttgtttctt ttttagtaat ttatggacat tgagatgaac 1632
 20 acaattgtga acttttgtga agattttatt tttaaacgtt tgaagtacta gtttttagttc 1692
 ttagcagagt agttttcaaa tatgattctt atgataaatg tagacacaaa ctatttgaga 1752
 aacatttga actcttagct tatacattca aaatgtaact attaaatgtg aagatttggg 1812
 25 gacaaaatgt gagtcagaca ctgaagagtt tttgttttg ttttaatatt tttgatattc 1872
 tctttgcatt gaaatggtat aaatgaatcc atttaaaaag tggtaagga tttgtttagc 1932
 30 tgggtgtgata ataattttta aagttgcaca ttgcccaagg ctttttttgt gtgtttttat 1992
 tgttgtttgt acatttgaaa aatattcttt gaataacctt gcagtactat atttcaagrt 2052
 ttctttataa atttaagtgc attttaactc ataattgtac actataatat aagcctaagt 2112
 35 ttttattcat aagttttatt gaagttctga tcgggtccct tcagaaattt ttttatatta 2172
 ttcttcaagt tactttctta tttatattgt atgtgcattt tatccattaa tgtttcatac 2232
 40 tttctgagag tataataccc ttttaaaaga tatttggtat accaatactt ttcttggtat 2292
 gaaaactttt tttaaacttt ttaaaatttg ggccactctg tatgcatatg tttggtcttg 2352
 ttaaagagga agaaaggatg tgtgttatac tgtacctgtg aatgttgata cagttacaat 2412
 45 ttatttgaca aggttgtaat tctagaatat gcttaataaa atgaaaactg gceatgacta 2472
 cagccagaac tgttatgaga ttaacatttc tattgagaag cttttgagta aagtactgta 2532
 50 tttgttcatg aagatgactg agatggtaac acttcgtgta gcttaaggaa atgggcagaa 2592
 tttcgtaa at gctgttggtc agatgtgttt tccctgaatg ctttcgtatt agtggcgacc 2652
 agtttctcac agaattgtga agcctgaagg ccaagaggaa gtcactgtta aaggactctg 2712

5 tgccatctta caaccttggg tgaattatcc tgccaacgtg aaaacctcat gttcaaagaa 2772
 cacttccctt tagccgatgt aactgctggg tttgtttttc atatgtgttt ttcttacact 2832
 catttgaatg ctttcaagca tttgttaaact taaaaaaaaa wawaaagggc aaaaagtctg 2892
 aacccttggt ttctgaaatc taatcagtta tgtatgggtt ctgaagggtg attttatttt 2952
 10 ggaataggta aagcgaaacc tgttttgtcw tgtttttctt gagggctaga tgcatttttt 3012
 ttctcacact cttaatgact tttaacattt atactgagca tccatagata tattcctaga 3072
 agtatgagaa gaattattct tattgaccat taatgtcatg ttcattttta tgtaatatata 3132
 15 ttgagatgaa atgttctctg gttggaacag atactctctt ttttttctt gcaatcttta 3192
 agaatacata gatctaaaat tcattagctt gaccctcaa agtaactttt aagtaaagat 3252
 20 taaagctttt cttctcagtg aatatatctg ctagaaggaa atagctggga agaattta 3312
 gatcaggga attcattatt tctatatgtg gaaactttt gcttcgaata ttgtatcttt 3372
 ttaaactctaa atgttcatat ttttctgaa gaaaccactg tgtaaaaatc aaattttaat 3432
 25 tttgaatgga ataatttcaa agaactatga agatgatttg aagctcta 3492
 acctataaaa tgttctttat atgtgttcat aagtaaattt tatattgatt aagttaaact 3552
 30 tttgaattga tttgaggagc agtaaaatga aagctatata tattnctaaa ccytatttag 3612
 acattggkac cagttacca ggtgaaaata kggagtaact ttgttttgta tggtaagggt 3672
 taggaatggn ggatgaaggg tatctctata taaataaagt gctcaacaat gtgcaatgat 3732
 35 tgtaaattta gtaagatatt acagccattt catgaatgct ttaccattca acatagtata 3792
 tattacaaaa cacctttctt gtatccatat acttcagggtg ttgctgttaa catttactat 3852
 40 gatatttatt ttaacaaaaa tggtactcac attaaatgtt tattctttta aatgaatgta 3912
 ttatgttttt aaccacaaa tgcatactta cctgtgcct catatttcaa tagtactgta 3972
 atatggacat cttttgtgaa atacttttat tttgttatgc tttaaata catacaaaaa 4032
 45 gatttctggt attagctttg aaaattgtat aatatactaa tataacaaaa atataaaaa 4092
 aaaaatgaat acagtaaaaa aaaaaaaaaa aaaaaaaaaa aaagg 4137

50

<210> 2
 <211> 302
 <212> PRT
 <213> Homo sapiens

- 84 -

<400> 2
 Met Asp Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
 1 5 10 15
 5 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
 20 25 30
 10 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
 35 40 45
 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
 50 55 60
 15 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
 65 70 75 80
 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
 85 90 95
 20 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
 100 105 110
 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
 115 120 125
 25 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
 130 135 140
 30 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
 145 150 155 160
 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
 165 170 175
 35 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
 180 185 190
 40 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
 195 200 205
 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
 210 215 220
 45 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
 225 230 235 240
 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
 245 250 255
 50 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
 260 265 270
 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val

275 280 285

Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
 290 295 300

5

<210> 3
 <211> 906
 <212> DNA
 10 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (906)

15

<400> 3
 atg gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc 48
 Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
 1 5 10 15

20

caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc 96
 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
 20 25 30

25

aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt 144
 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
 35 40 45

30

tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa 192
 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
 50 55 60

35

gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc 240
 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
 65 70 75 80

40

aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa 288
 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
 85 90 95

45

tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa 336
 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
 100 105 110

50

cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag 384
 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
 115 120 125

caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag 432
 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
 130 135 140

ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga 480
 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg

- 86 -

	145		150		155		160	
	gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa							528
	Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys							
5		165			170		175	
	ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct							576
	Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala							
		180			185		190	
10								
	gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata							624
	Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile							
		195			200		205	
15								
	cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt							672
	His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys							
		210			215		220	
	cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa							720
20	Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys							
		225			230		235	240
	atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca							768
	Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro							
25		245			250		255	
	cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat							816
	Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn							
		260			265		270	
30								
	atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt							864
	Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val							
		275			280		285	
35								
	tat gac gta gca aag agg atg cat gca tgc act gca agc agc							906
	Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser							
		290			295		300	
40	<210> 4							
	<211> 2120							
	<212> DNA							
	<213> Homo sapiens							
45	<220>							
	<221> CDS							
	<222> (47)..(1411)							
	<400> 4							
50	gtcgacccac gcgtccggtg gaagtataat actttgtcat tatgag atg tcg tct							55
							Met Ser Ser	
							1	
	ctc ggt gcc tcc ttt gtg caa att aaa ttt gat gac ttg cag ttt ttt							103

- 87 -

	Leu	Gly	Ala	Ser	Phe	Val	Gln	Ile	Lys	Phe	Asp	Asp	Leu	Gln	Phe	Phe	
	5						10					15					
5	gaa	aac	tgc	ggt	gga	gga	agt	ttt	ggg	agt	gtt	tat	cga	gcc	aaa	tgg	151
	Glu	Asn	Cys	Gly	Gly	Gly	Ser	Phe	Gly	Ser	Val	Tyr	Arg	Ala	Lys	Trp	
	20					25					30				35		
10	ata	tca	cag	gac	aag	gag	gtg	gct	gta	aag	aag	ctc	ctc	aaa	ata	gag	199
	Ile	Ser	Gln	Asp	Lys	Glu	Val	Ala	Val	Lys	Lys	Leu	Leu	Lys	Ile	Glu	
					40					45					50		
15	aaa	gag	gca	gaa	ata	ctc	agt	gtc	ctc	agt	cac	aga	aac	atc	atc	cag	247
	Lys	Glu	Ala	Glu	Ile	Leu	Ser	Val	Leu	Ser	His	Arg	Asn	Ile	Ile	Gln	
				55					60					65			
20	ttt	tat	gga	gta	att	ctt	gaa	cct	ccc	aac	tat	ggc	att	gtc	aca	gaa	295
	Phe	Tyr	Gly	Val	Ile	Leu	Glu	Pro	Pro	Asn	Tyr	Gly	Ile	Val	Thr	Glu	
			70					75					80				
25	tat	gct	tct	ctg	gga	tca	ctc	tat	gat	tac	att	aac	agt	aac	aga	agt	343
	Tyr	Ala	Ser	Leu	Gly	Ser	Leu	Tyr	Asp	Tyr	Ile	Asn	Ser	Asn	Arg	Ser	
		85					90					95					
30	gag	gag	atg	gat	atg	gat	cac	att	atg	acc	tgg	gcc	act	gat	gta	gcc	391
	Glu	Glu	Met	Asp	Met	Asp	His	Ile	Met	Thr	Trp	Ala	Thr	Asp	Val	Ala	
	100					105					110				115		
35	aaa	gga	atg	cat	tat	tta	cat	atg	gag	gct	cct	gtc	aag	gtg	att	cac	439
	Lys	Gly	Met	His	Tyr	Leu	His	Met	Glu	Ala	Pro	Val	Lys	Val	Ile	His	
					120					125					130		
40	aga	gac	ctc	aag	tca	aga	aac	gtt	gtt	ata	gct	gct	gat	gga	gta	ctg	487
	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Val	Ile	Ala	Ala	Asp	Gly	Val	Leu	
				135					140					145			
45	aag	atc	tgt	gac	ttt	ggt	gcc	tct	cgg	ttc	cat	aac	cat	aca	aca	cac	535
	Lys	Ile	Cys	Asp	Phe	Gly	Ala	Ser	Arg	Phe	His	Asn	His	Thr	Thr	His	
		150					155					160					
50	atg	tcc	ttg	gtt	gga	act	ttc	cca	tgg	atg	gct	cca	gaa	gtt	atc	cag	583
	Met	Ser	Leu	Val	Gly	Thr	Phe	Pro	Trp	Met	Ala	Pro	Glu	Val	Ile	Gln	
		165					170					175					
55	agt	ctc	cct	gtg	tca	gaa	act	tgt	gac	aca	tat	tcc	tat	ggg	gtg	gtt	631
	Ser	Leu	Pro	Val	Ser	Glu	Thr	Cys	Asp	Thr	Tyr	Ser	Tyr	Gly	Val	Val	
	180					185				190					195		
60	ctc	tgg	gag	atg	cta	aca	agg	gag	gtc	ccc	ttt	aaa	ggg	ttg	gaa	gga	679
	Leu	Trp	Glu	Met	Leu	Thr	Arg	Glu	Val	Pro	Phe	Lys	Gly	Leu	Glu	Gly	
					200					205				210			
65	tta	caa	gta	gct	tgg	ctt	gta	gtg	gaa	aaa	aac	gag	aga	tta	acc	att	727
	Leu	Gln	Val	Ala	Trp	Leu	Val	Val	Glu	Lys	Asn	Glu	Arg	Leu	Thr	Ile	
				215					220					225			

cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat cag tgt tgg 775
Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His Gln Cys Trp
230 235 240

5 gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc att tca atc 823
Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile Ile Ser Ile
245 250 255

10 ctg gag tcc atg tca aat gac acg agc ctt cct gac aag tgt tac tca 871
Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys Cys Asn Ser
260 265 270 275

15 ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag gca act ctt 919
Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu Ala Thr Leu
280 285 290

20 gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag gag cag gag 967
Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys Glu Gln Glu
295 300 305

ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa aag ctg aca 1015
Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln Lys Leu Thr
310 315 320

25 gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca aga atg tct 1063
Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala Arg Met Ser
325 330 335

30 gag gag tct tac ttt gaa tct aaa aca gag gag tca aac agt gca gag 1111
Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn Ser Ala Glu
340 345 350 355

35 atg tca tgt cag atc aca gca aca agt aac ggg gag ggc cat ggc atg 1159
Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly His Gly Met
360 365 370

aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg gat atc ttc 1207
Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly Asp Ile Phe
375 380 385

40 tca atg aac aaa gca gga gct gtg atg cat tct ggg atg cag ata aac 1255
Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met Gln Ile Asn
390 395 400

45 atg caa gcc aag cag aat tct tcc aaa acc aca tct aag aga agg ggg 1303
Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys Arg Arg Gly
405 410 415

50 aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac ttg tca gaa 1351
Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp Leu Ser Glu
420 425 430 435

ggg gac gat gat gat gat gat gac ggt gag gag gag gat aat gac atg 1399

- 89 -

Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp Asn Asp Met
440 445 450

gat aat agt gaa tgaaagcaga aagcaaagta ataaaatcac aaatgtttgg 1451
5 Asp Asn Ser Glu
455

aaaacacaaa agtaacttgt ttatctcagt ctgtacaaaa acagtaagga ggcagaaagc 1511

10 caagcactgc attttttaggc caatcacatt tacatgaccg taatttctta tcaattctac 1571

ttttatTTTT gcttacagaa aaacgggggg agaattaagc caaagaagta tatttatgaa 1631

tcagcaaatg tgggtgcctga ttatagaaat ttgtgatcct atatacaata taggactttt 1691

15 aaagtgtgta cattctggct ttttctttta atgaatactt tttagtttgt atttgacttt 1751

atttccttta ttcaaatcat ttttaaaaac ttacattttg aacaaacact cttaactcct 1811

20 aattgttctt tgacacgtag taattctgtg acatactttt tttttcttat agcaatacac 1871

tgtaatatca gaaatggttg gctgagcaa cctagtaaga cctcgtctct actaataatt 1931

aaaaaactag ctggcatggt agcacacacc tgtagtcca gatacttggg aggccaaggc 1991

25 aggaggattg cttgagacct agcaatcagt cagggctgca gtgagccatg atggcaccac 2051

tgcactctag cctgggcaag agaacaagat cctgtctcaa aaaacaaaaa aaaaaaaaaa 2111

30 gggcggccg 2120

<210> 5
<211> 455
35 <212> PRT
<213> Homo sapiens

<400> 5

Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu
40 1 5 10 15

Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg
20 25 30

45 Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu
35 40 45

Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn
50 55 60

50 Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile
65 70 75 80

Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser

- 90 -

					85					90					95					
					Asn	Arg	Ser	Glu	Glu	Met	Asp	Met	Asp	His	Ile	Met	Thr	Trp	Ala	Thr
								100					105					110		
5					Asp	Val	Ala	Lys	Gly	Met	His	Tyr	Leu	His	Met	Glu	Ala	Pro	Val	Lys
								115					120				125			
					Val	Ile	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Val	Ile	Ala	Ala	Asp
10								130					135				140			
					Gly	Val	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Ala	Ser	Arg	Phe	His	Asn	His
								145							155					160
15					Thr	Thr	His	Met	Ser	Leu	Val	Gly	Thr	Phe	Pro	Trp	Met	Ala	Pro	Glu
								165						170						175
					Val	Ile	Gln	Ser	Leu	Pro	Val	Ser	Glu	Thr	Cys	Asp	Thr	Tyr	Ser	Tyr
20								180					185					190		
					Gly	Val	Val	Leu	Trp	Glu	Met	Leu	Thr	Arg	Glu	Val	Pro	Phe	Lys	Gly
								195					200				205			
					Leu	Glu	Gly	Leu	Gln	Val	Ala	Trp	Leu	Val	Val	Glu	Lys	Asn	Glu	Arg
25								210				215				220				
					Leu	Thr	Ile	Pro	Ser	Ser	Cys	Pro	Arg	Ser	Phe	Ala	Glu	Leu	Leu	His
								225				230			235					240
30					Gln	Cys	Trp	Glu	Ala	Asp	Ala	Lys	Lys	Arg	Pro	Ser	Phe	Lys	Gln	Ile
								245						250						255
					Ile	Ser	Ile	Leu	Glu	Ser	Met	Ser	Asn	Asp	Thr	Ser	Leu	Pro	Asp	Lys
35								260					265					270		
					Cys	Asn	Ser	Phe	Leu	His	Asn	Lys	Ala	Glu	Trp	Arg	Cys	Glu	Ile	Glu
								275				280					285			
40					Ala	Thr	Leu	Glu	Arg	Leu	Lys	Lys	Leu	Glu	Arg	Asp	Leu	Ser	Phe	Lys
								290				295				300				
					Glu	Gln	Glu	Leu	Lys	Glu	Arg	Glu	Arg	Arg	Leu	Lys	Met	Trp	Glu	Gln
								305							315					320
45					Lys	Leu	Thr	Glu	Gln	Ser	Asn	Thr	Pro	Leu	Leu	Leu	Pro	Leu	Ala	Ala
								325						330						335
					Arg	Met	Ser	Glu	Glu	Ser	Tyr	Phe	Glu	Ser	Lys	Thr	Glu	Glu	Ser	Asn
50								340					345					350		
					Ser	Ala	Glu	Met	Ser	Cys	Gln	Ile	Thr	Ala	Thr	Ser	Asn	Gly	Glu	Gly
								355					360				365			
					His	Gly	Met	Asn	Pro	Ser	Leu	Gln	Ala	Met	Met	Leu	Met	Gly	Phe	Gly

- 91 -

370 375 380
 Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met
 385 390 395 400
 5 Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys
 405 410 415
 10 Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp
 420 425 430
 Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp
 435 440 445
 15 Asn Asp Met Asp Asn Ser Glu
 450 455

 20 <210> 6
 <211> 1365
 <212> DNA
 <213> Homo sapiens

 25 <220>
 <221> CDS
 <222> (1)..(1365)

 <400> 6
 30 atg tcg tct ctc ggt gcc tcc ttt gtg caa att aaa ttt gat gac ttg 48
 Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu
 1 5 10 15
 cag ttt ttt gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga 96
 Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg
 35 20 25 30
 gcc aaa tgg ata tca cag gac aag gag gtg gct gta aag aag ctc ctc 144
 Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu
 35 40 45
 40 aaa ata gag aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac 192
 Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn
 50 55 60
 45 atc atc cag ttt tat gga gta att ctt gaa cct ccc aac tat ggc att 240
 Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile
 65 70 75 80
 gtc aca gaa tat gct tct ctg gga tca ctc tat gat tac att aac agt 288
 50 Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser
 85 90 95
 aac aga agt gag gag atg gat atg gat cac att atg acc tgg gcc act 336
 Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr

- 92 -

	100	105	110	
5	gat gta gcc aaa gga atg cat tat tta cat atg gag gct cct gtc aag Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys 115 120 125	384		
10	gtg att cac aga gac ctc aag tca aga aac gtt gtt ata gct gct gat Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp 130 135 140	432		
15	gga gta ctg aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His 145 150 155 160	480		
20	aca aca cac atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu 165 170 175	528		
25	gtt atc cag agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr 180 185 190	576		
30	ggt gtg gtt ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly 195 200 205	624		
35	ttg gaa gga tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg 210 215 220	672		
40	tta acc att cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His 225 230 235 240	720		
45	cag tgt tgg gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile 245 250 255	768		
50	att tca atc ctg gag tcc atg tca aat gac acg agc ctt cct gac aag Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys 260 265 270	816		
55	tgt aac tca ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu 275 280 285	864		
60	gca act ctt gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys 290 295 300	912		
65	gag cag gag ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln 305 310 315 320	960		

- 94 -

	ctg cgc ttc acg ggc aag ccc ggc cgg gcc tac ggc ttg ggg cgg ccg	152
	Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro	
	20 25 30	
5	ggc ccg gcg gcg ggc tgt gtc cgc ggg gag cgt cca ggc tgg gcc gca	200
	Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala	
	35 40 45 50	
10	gga ccg ggc gcg gag cct cgc agg gtc ggg ctc ggg ctt cct aac cgt	248
	Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg	
	55 60 65	
15	ctc cgc ttc ttc cgc cag tcg gtg gcc ggg ctg gcg gcg cgg ttg cag	296
	Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln	
	70 75 80	
20	cgg cag ttc gtg gtg cgg gcc tgg ggc tgc gcg ggc cct tgc ggc cgg	344
	Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg	
	85 90 95	
25	gca gtc ttt ctg gcc ttc ggg cta ggg ctg ggc ctc atc gag gaa aaa	392
	Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys	
	100 105 110	
30	cag gcg gag agc cgg cgg gcg gtc tcg gcc tgt cag gag atc cag gca	440
	Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala	
	115 120 125 130	
35	att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac acg aga	488
	Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg	
	135 140 145	
40	cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag tcc att	536
	Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile	
	150 155 160	
45	ggc cca ggt acc agt gca cca gga gaa ggg cag gag cga gct ceg ggg	680
	Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly	
	195 200 205 210	
50	gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc tcg gca	728
	Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala	
	215 220 225	
	ggc tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag ctg gtc	776

- 95 -

	Gly	Ser	Ser	Ser	Glu	Ala	Ile	Leu	Asn	Thr	Met	Ser	Gln	Glu	Leu	Val	
				230					235					240			
5	cca	gcg	agc	cga	gtg	gcc	ttg	gct	ggg	gag	tat	gga	gca	gtc	act	tac	824
	Pro	Ala	Ser	Arg	Val	Ala	Leu	Ala	Gly	Glu	Tyr	Gly	Ala	Val	Thr	Tyr	
			245				250					255					
10	aga	aaa	tcc	aag	aga	ggt	ccc	aag	caa	cta	gcc	cct	cac	ccc	aac	atc	872
	Arg	Lys	Ser	Lys	Arg	Gly	Pro	Lys	Gln	Leu	Ala	Pro	His	Pro	Asn	Ile	
		260				265					270						
15	atc	cgg	gtt	ctc	cgc	gcc	ttc	acc	tct	tcc	gtg	ccg	ctg	ctg	cca	ggg	920
	Ile	Arg	Val	Leu	Arg	Ala	Phe	Thr	Ser	Ser	Val	Pro	Leu	Leu	Pro	Gly	
	275					280					285					290	
20	gcc	ctg	gtc	gac	tac	cct	gat	gtg	ctg	ccc	tca	cgc	ctc	cac	cct	gaa	968
	Ala	Leu	Val	Asp	Tyr	Pro	Asp	Val	Leu	Pro	Ser	Arg	Leu	His	Pro	Glu	
				295					300						305		
25	ggc	ctg	ggc	cat	ggc	cgg	acg	ctg	ttc	ctc	gtt	atg	aag	aac	tat	ccc	1016
	Gly	Leu	Gly	His	Gly	Arg	Thr	Leu	Phe	Leu	Val	Met	Lys	Asn	Tyr	Pro	
				310				315						320			
30	tgt	acc	ctg	cgc	cag	tac	ctt	tgt	gtg	aac	aca	ccc	agc	ccc	cgc	ctc	1064
	Cys	Thr	Leu	Arg	Gln	Tyr	Leu	Cys	Val	Asn	Thr	Pro	Ser	Pro	Arg	Leu	
			325				330					335					
35	gcc	gcc	atg	atg	ctg	ctg	cag	ctg	ctg	gaa	ggc	gtg	gac	cat	ctg	gtt	1112
	Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His	Leu	Val	
		340				345				350							
40	caa	cag	ggc	atc	gcg	cac	aga	gac	ctg	aaa	tcc	gac	aac	atc	ctt	gtg	1160
	Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile	Leu	Val	
	355				360				365						370		
45	gag	ctg	gac	cca	gac	ggc	tgc	ccc	tgg	ctg	gtg	atc	gca	gat	ttt	ggc	1208
	Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp	Phe	Gly	
				375			380							385			
50	tgc	tgc	ctg	gct	gat	gag	agc	atc	ggc	ctg	cag	ttg	ccc	ttc	agc	agc	1256
	Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe	Ser	Ser	
				390			395						400				
55	tgg	tac	gtg	gat	cgg	ggc	gga	aac	ggc	tgt	ctg	atg	gcc	cca	gag	gtg	1304
	Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro	Glu	Val	
			405			410						415					
60	tcc	acg	gcc	cgt	cct	ggc	ccc	agg	gca	gtg	att	gac	tac	agc	aag	gct	1352
	Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser	Lys	Ala	
		420				425					430						
65	gat	gcc	tgg	gca	gtg	gga	gcc	atc	gcc	tat	gaa	atc	ttc	ggg	ctt	gtc	1400
	Asp	Ala	Trp	Ala	Val	Gly	Ala	Ile	Ala	Tyr	Glu	Ile	Phe	Gly	Leu	Val	
	435				440				445						450		

- 96 -

aat ccc ttc tac ggc cag ggc aag gcc cac ctt gaa agc cgc agc tac 1448
 Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
 455 460 465

5

caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca gac gtg 1496
 Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
 470 475 480

10

aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag aga cca 1544
 Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
 485 490 495

15

tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg ggt gaa 1592
 Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
 500 505 510

20

cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt ggc tgg 1640
 His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
 515 520 525 530

25

ctc ctc caa caa tcg gcc gcc act ttg ttg gcc aac agg ctc aca gag 1688
 Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
 535 540 545

aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct aac ctg 1736
 Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
 550 555 560

30

gag tgt gaa acg ctc tgc cag gca gcc ctc ctc ctc tgc tca tgg agg 1784
 Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
 565 570 575

35

gca gcc ctg tgatgtccct gcatggagct ggtgaattac taaaagaact 1833
 Ala Ala Leu
 580

40

tggcatcctc tgtgtcgtga tggctctgtga atggtgaggg tgggagtcag gagacaagac 1893
 agcgcagaga gggctgggta gccggaagag gcctcgggct tggcaaatgg aagaacttga 1953
 gtgagagttc agtctgcagt cctctgctca cagacatctg aaaagtgaat ggccaagctg 2013
 gtctagtaga tgaggctgga ctgaggaggg gtaggcctgc atccacagag aggatccagg 2073

45

ccaaggcact ggctgtcagt ggcagagttt ggctgtgacc tttgcccta acacgaggaa 2133
 ctcgtttgaa gggggcagcg tagcatgtct gatttgccac ctggatgaag gcagacatca 2193

50

acatgggtca gcacgttcag ttacgggagt gggaaattac atgaggcctg ggctctgctg 2253
 ttcccaagct gtgcgttctg gaccagctac tgaattatta atctcactta gcgaaagtga 2313
 cggatgagca gtaagtaagt aagtgtgggg atttaaactt gagggtttcc ctctgacta 2373

- 97 -

gcctctcttta ccaggaattgt gaaatatttaa atgcaaattt acaactgcaa aaaaaaaaaa 2433

aaaaaaaaaa aagggcggcc c 2454

5

<210> 8

<211> 581

<212> PRT

10 <213> Homo sapiens

<400> 8

Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala
1 5 10 15

15

Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly
20 25 30

20

Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp
35 40 45

Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro
50 55 60

25

Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg
65 70 75 80

Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
85 90 95

30

Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu
100 105 110

35

Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile
115 120 125

Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp
130 135 140

40

Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln
145 150 155 160

Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro
165 170 175

45

Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro
180 185 190

50

Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala
195 200 205

Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile
210 215 220

- 98 -

	Ser	Ala	Gly	Ser	Ser	Ser	Glu	Ala	Ile	Leu	Asn	Thr	Met	Ser	Gln	Glu	
	225					230					235					240	
5	Leu	Val	Pro	Ala	Ser	Arg	Val	Ala	Leu	Ala	Gly	Glu	Tyr	Gly	Ala	Val	
					245				250						255		
	Thr	Tyr	Arg	Lys	Ser	Lys	Arg	Gly	Pro	Lys	Gln	Leu	Ala	Pro	His	Pro	
				260					265					270			
10	Asn	Ile	Ile	Arg	Val	Leu	Arg	Ala	Phe	Thr	Ser	Ser	Val	Pro	Leu	Leu	
		275						280					285				
	Pro	Gly	Ala	Leu	Val	Asp	Tyr	Pro	Asp	Val	Leu	Pro	Ser	Arg	Leu	His	
		290					295					300					
15	Pro	Glu	Gly	Leu	Gly	His	Gly	Arg	Thr	Leu	Phe	Leu	Val	Met	Lys	Asn	
	305					310					315					320	
	Tyr	Pro	Cys	Thr	Leu	Arg	Gln	Tyr	Leu	Cys	Val	Asn	Thr	Pro	Ser	Pro	
20					325					330					335		
	Arg	Leu	Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His	
				340					345					350			
25	Leu	Val	Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile	
		355						360					365				
	Leu	Val	Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp	
		370					375					380					
30	Phe	Gly	Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe	
	385					390					395					400	
	Ser	Ser	Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro	
35					405					410					415		
	Glu	Val	Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser	
				420					425					430			
40	Lys	Ala	Asp	Ala	Trp	Ala	Val	Gly	Ala	Ile	Ala	Tyr	Glu	Ile	Phe	Gly	
		435						440					445				
	Leu	Val	Asn	Pro	Phe	Tyr	Gly	Gln	Gly	Lys	Ala	His	Leu	Glu	Ser	Arg	
		450					455					460					
45	Ser	Tyr	Gln	Glu	Ala	Gln	Leu	Pro	Ala	Leu	Pro	Glu	Ser	Val	Pro	Pro	
	465					470					475					480	
	Asp	Val	Arg	Gln	Leu	Val	Arg	Ala	Leu	Leu	Gln	Arg	Glu	Ala	Ser	Lys	
50					485					490					495		
	Arg	Pro	Ser	Ala	Arg	Val	Ala	Ala	Asn	Val	Leu	His	Leu	Ser	Leu	Trp	
				500					505					510			

	Gly	Glu	His	Ile	Leu	Ala	Leu	Lys	Asn	Leu	Lys	Leu	Asp	Lys	Met	Val		
	515							520						525				
5	Gly	Trp	Leu	Leu	Gln	Gln	Ser	Ala	Ala	Thr	Leu	Leu	Ala	Asn	Arg	Leu		
	530							535						540				
	Thr	Glu	Lys	Cys	Cys	Val	Glu	Thr	Lys	Met	Lys	Met	Leu	Phe	Leu	Ala		
	545							550						555				560
10	Asn	Leu	Glu	Cys	Glu	Thr	Leu	Cys	Gln	Ala	Ala	Leu	Leu	Leu	Cys	Ser		
	565							570						575				
	Trp	Arg	Ala	Ala	Leu													
	580																	
15																		
	<210> 9																	
	<211> 1743																	
	<212> DNA																	
20	<213> Homo sapiens																	
	<220>																	
	<221> CDS																	
	<222> (1) .. (1743)																	
25																		
	<400> 9																	
	atg	gcg	gtg	cga	cag	gcg	ctg	ggc	cgc	ggc	ctg	cag	ctg	ggt	cga	gcg	48	
	Met	Ala	Val	Arg	Gln	Ala	Leu	Gly	Arg	Gly	Leu	Gln	Leu	Gly	Arg	Ala		
	1				5					10					15			
30																		
	ctg	ctg	ctg	cgc	ttc	acg	ggc	aag	ccc	ggc	cgg	gcc	tac	ggc	ttg	ggg	96	
	Leu	Leu	Leu	Arg	Phe	Thr	Gly	Lys	Pro	Gly	Arg	Ala	Tyr	Gly	Leu	Gly		
				20					25					30				
35																		
	cgg	ccg	ggc	ccg	gcg	gcg	ggc	tgt	gtc	cgc	ggg	gag	cgt	cca	ggc	tgg	144	
	Arg	Pro	Gly	Pro	Ala	Ala	Gly	Cys	Val	Arg	Gly	Glu	Arg	Pro	Gly	Trp		
			35					40					45					
40																		
	gcc	gca	gga	ccg	ggc	gcg	gag	cct	cgc	agg	gtc	ggg	ctc	ggg	ctt	cct	192	
	Ala	Ala	Gly	Pro	Gly	Ala	Glu	Pro	Arg	Arg	Val	Gly	Leu	Gly	Leu	Pro		
			50					55					60					
45																		
	aac	cgt	ctc	cgc	ttc	ttc	cgc	cag	tcg	gtg	gcc	ggg	ctg	gcg	gcg	cgg	240	
	Asn	Arg	Leu	Arg	Phe	Phe	Arg	Gln	Ser	Val	Ala	Gly	Leu	Ala	Ala	Arg		
	65					70					75					80		
50																		
	ttg	cag	cgg	cag	ttc	gtg	gtg	cgg	gcc	tgg	ggc	tgc	gcg	ggc	cct	tgc	288	
	Leu	Gln	Arg	Gln	Phe	Val	Val	Arg	Ala	Trp	Gly	Cys	Ala	Gly	Pro	Cys		
					85					90					95			
55																		
	ggc	cgg	gca	gtc	ttt	ctg	gcc	ttc	ggg	cta	ggg	ctg	ggc	ctc	atc	gag	336	
	Gly	Arg	Ala	Val	Phe	Leu	Ala	Phe	Gly	Leu	Gly	Leu	Gly	Leu	Ile	Glu		
					100				105						110			

- 100 -

	gaa aaa cag gcg gag agc cgg cgg gcg gtc tcg gcc tgt cag gag atc	384
	Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile	
	115 120 125	
5	cag gca att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac	432
	Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp	
	130 135 140	
10	acg aga cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag	480
	Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln	
	145 150 155 160	
15	tcc att ggt aag ggc tgc agt gct gct gtg tat gaa gcc acc atg cct	528
	Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro	
	165 170 175	
20	aca ttg ccc cag aac ctg gag gtg aca aag agc acc ggg ttg ctt cca	576
	Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro	
	180 185 190	
25	ggg aga ggc cca ggt acc agt gca cca gga gaa ggg cag gag cga gct	624
	Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala	
	195 200 205	
30	ccg ggg gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc	672
	Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile	
	210 215 220	
35	tcg gca ggt tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag	720
	Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu	
	225 230 235 240	
40	ctg gtc cca gcg agc cga gtg gcc ttg gct ggg gag tat gga gca gtc	768
	Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val	
	245 250 255	
45	act tac aga aaa tcc aag aga ggt ccc aag caa cta gcc cct cac ccc	816
	Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro	
	260 265 270	
50	aac atc atc cgg gtt ctc cgc gcc ttc acc tct tcc gtg ccg ctg ctg	864
	Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu	
	275 280 285	
55	cca ggg gcc ctg gtc gac tac cct gat gtg ctg ccc tca cgc ctc cac	912
	Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His	
	290 295 300	
60	cct gaa ggc ctg ggc cat ggc cgg acg ctg ttc ctc gtt atg aag aac	960
	Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn	
	305 310 315 320	
65	tat ccc tgt acc ctg cgc cag tac ctt tgt gtg aac aca ccc agc ccc	1008
	Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro	

- 101 -

	325	330	335	
5	cgc ctc gcc gcc atg atg ctg ctg cag ctg ctg gaa ggc gtg gac cat Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His 340 345 350	1056		
10	ctg gtt caa cag ggc atc gcg cac aga gac ctg aaa tcc gac aac atc Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile 355 360 365	1104		
15	ctt gtg gag ctg gac cca gac ggc tgc ccc tgg ctg gtg atc gca gat Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp 370 375 380	1152		
20	ttt ggc tgc tgc ctg gct gat gag agc atc ggc ctg cag ttg ccc ttc Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe 385 390 395 400	1200		
25	agc agc tgg tac gtg gat cgg ggc gga aac ggc tgt ctg atg gcc cca Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro 405 410 415	1248		
30	gag gtg tcc acg gcc cgt cct ggc ccc agg gca gtg att gac tac agc Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser 420 425 430	1296		
35	aag gct gat gcc tgg gca gtg gga gcc atc gcc tat gaa atc ttc ggg Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly 435 440 445	1344		
40	ctt gtc aat ccc ttc tac ggc cag ggc aag gcc cac ctt gaa agc cgc Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg 450 455 460	1392		
45	agc tac caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro 465 470 475 480	1440		
50	gac gtg aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys 485 490 495	1488		
55	aga cca tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp 500 505 510	1536		
60	ggc gaa cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val 515 520 525	1584		
65	ggc tgg ctc ctc caa caa tgc gcc gcc act ttg ttg gcc aac agg ctc Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu 530 535 540	1632		

- 102 -

aca gag aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct 1680
 Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala
 545 550 555 560

5 aac ctg gag tgt gaa acg ctc tgc cag gca gcc ctc ctc ctc tgc tca 1728
 Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser
 565 570 575

10 tgg agg gca gcc ctg 1743
 Trp Arg Ala Ala Leu
 580

15 <210> 10
 <211> 1864
 <212> DNA
 <213> Homo sapiens

20 <220>
 <221> CDS
 <222> (275) .. (754)

25 <400> 10
 gtcgacccac gcggtccgcc cacgcgttcc ggagacatgt ctctgtgttt ctctcccctc 60
 cgcttttgag tccgttgaag acacaatttc tctctgtcgg gtgcttagga ggagctccat 120
 gaacatgtat tgaattggac ttagctgaac aggctgctgg ttggctgccc agaggggggca 180
 30 ggctgtgttg ctgggagcct tccagctccc tgcagcagtc atggggcagg gttccccgag 240
 tccgtaatcc ccatttccac ctactttccc ttag tta ttt gat tcc ctg tct gtc 295
 Leu Phe Asp Ser Leu Ser Val
 1 5

35 gta ctc agc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag 343
 Val Leu Ser Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
 10 15 20

40 gaa aca ctg gca aat atc aca gca gtg agt tac gac ttt gat gag gaa 391
 Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
 25 30 35

45 ttc ttc agc cag acg agc gag ctg gcc aag gac ttt att cgg aag ctt 439
 Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
 40 45 50 55

50 ctg gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga 487
 Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
 60 65 70

cac ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cgc agg 535
 His Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg
 75 80 85

- 103 -

gag tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg 583
 Glu Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg
 90 95 100

5 cgg tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc 631
 Arg Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr
 105 110 115

10 cgc tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg 679
 Arg Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg
 120 125 130 135

15 aac tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc 727
 Asn Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu
 140 145 150

20 cac cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt 774
 His Pro Arg Arg Arg Ser Ser Thr Ser
 155 160

25 ggccgccagg gaggtctggg cccagcgggg ctcccttctg tgcagacttt tggacccagc 834
 tcagcaccag caccggggcg tcctgagcac ttgcaagag agatgggccc aaggaattca 894
 gaagagcttg caggcaagcc aggagaccct gggagctgtg gctgtcttct gtggaggagg 954
 ctccagcatt cccaaagctc ttaattctcc ataaaatggg ctttctctg tctgccatcc 1014

30 tcagagtctg ggggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc 1074
 acgggggtgaa ggtcagacta aggcagcctt cttcacaggc tgaggggggtt cagaaccagc 1134
 ctggccaaaa attacaccag agagacagag tcctcccat tgggaacagg gtgattgagg 1194

35 aaagtgaacc ttgggtgtga gggaccaatc ctgtgacctc ccagaaccat ggaagccagg 1254
 acgtcaggct gaccaacacc tcagaccttc tgaagcagcc cattgctggc ccgccatgtt 1314

40 gtaattttgc tcatttttat taaacttctg gtttacctga tgcttggtt cttttagggc 1374
 taccctcatc tcatttcctt tagccctgtg gcctgtaact ctgagggggg gcacccagt 1434
 ggggtgctgag tgggcagaat ctcagaaggc cctcctgaac cgtccgcgca ggctgcagt 1494

45 gggcctgcct cctccttgct tcctaacag gaaggtgtcc agttcaagag aaccaccca 1554
 gagactggga gtggtggctc acgcctataa tcctgcgct ttggcagtcc gaggcagggg 1614

50 aattgcttga actcaggagt tggagaccag cctgggcaac atggcaaac gcagtctgta 1674
 caaaaaatac aaaaaattag ccaggtgtag gggtaggcac ctggcatccc agctactcca 1734
 ggggctgagg tgacagcatt gcttaagccc agaaggtcga ggctgcagtg agctgagatc 1794

- 104 -

acgccactgcactccagtct gggtgacaga gagagaccat atccaaaaaa aaaaaaaaaa 1854
 gggcggccgc 1864

5

<210> 11
 <211> 160
 <212> PRT
 10 <213> Homo sapiens

<400> 11
 Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro
 1 5 10 15

15 Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
 20 25 30

20 Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
 35 40 45

Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
 50 55 60

25 Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn
 65 70 75 80

Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe
 85 90 95

30 Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val
 100 105 110

35 Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu
 115 120 125

Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp
 130 135 140

40 Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser
 145 150 155 160

<210> 12
 45 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 50 <221> CDS
 <222> (1)..(480)

<400> 12
 tta ttt gat tcc ctg tct gtc gta ctc agc tta agt gga gca tcc cct 48

- 105 -

	Leu	Phe	Asp	Ser	Leu	Ser	Val	Val	Leu	Ser	Leu	Ser	Gly	Ala	Ser	Pro	
	1				5					10					15		
	ttc	ctg	gga	gac	acg	aag	cag	gaa	aca	ctg	gca	aat	atc	aca	gca	gtg	96
5	Phe	Leu	Gly	Asp	Thr	Lys	Gln	Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	
				20					25					30			
	agt	tac	gac	ttt	gat	gag	gaa	ttc	ttc	agc	cag	acg	agc	gag	ctg	gcc	144
10	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	
			35					40					45				
	aag	gac	ttt	att	cgg	aag	ctt	ctg	gtt	aaa	gag	acc	cgg	aaa	cgg	ctc	192
	Lys	Asp	Phe	Ile	Arg	Lys	Leu	Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	
15			50				55					60					
	aca	atc	caa	gag	gct	ctc	aga	cac	ccc	tgg	atc	acg	ccg	gtg	gac	aac	240
	Thr	Ile	Gln	Glu	Ala	Leu	Arg	His	Pro	Trp	Ile	Thr	Pro	Val	Asp	Asn	
			65			70				75					80		
20	cag	caa	gcc	atg	gtg	cgc	agg	gag	tct	gtg	gtc	aat	ctg	gag	aac	ttc	288
	Gln	Gln	Ala	Met	Val	Arg	Arg	Glu	Ser	Val	Val	Asn	Leu	Glu	Asn	Phe	
					85					90					95		
	agg	aag	cag	tat	gtc	cgc	agg	cgg	tgg	aag	ctt	tcc	ttc	agc	atc	gtg	336
25	Arg	Lys	Gln	Tyr	Val	Arg	Arg	Arg	Trp	Lys	Leu	Ser	Phe	Ser	Ile	Val	
				100					105					110			
	tcc	ctg	tgc	aac	cac	ctc	acc	cgc	tcg	ctg	atg	aag	aag	gtg	cac	ctg	384
30	Ser	Leu	Cys	Asn	His	Leu	Thr	Arg	Ser	Leu	Met	Lys	Lys	Val	His	Leu	
			115					120					125				
	agg	ccg	gat	gag	gac	ctg	agg	aac	tgt	gag	agt	gac	act	gag	gag	gac	432
	Arg	Pro	Asp	Glu	Asp	Leu	Arg	Asn	Cys	Glu	Ser	Asp	Thr	Glu	Glu	Asp	
35			130				135					140					
	atc	gcc	agg	agg	aaa	gcc	ctc	cac	cca	cgg	agg	agg	agc	agc	acc	tcc	480
	Ile	Ala	Arg	Arg	Lys	Ala	Leu	His	Pro	Arg	Arg	Arg	Ser	Ser	Thr	Ser	
	145					150				155					160		
40																	
	<210>	13															
	<211>	1333															
	<212>	DNA															
	<213>	Homo sapiens															
45																	
	<220>																
	<221>	CDS															
	<222>	(2) .. (1333)															
50																	
	<400>	13															
	g	acg	gca	tta	gcc	aaa	gaa	cta	aga	gaa	ctc	cgg	att	gaa	gaa	aca	49
	Thr	Ala	Leu	Ala	Lys	Glu	Leu	Arg	Glu	Leu	Arg	Ile	Glu	Glu	Thr	Asn	
	1					5					10				15		

- 106 -

	cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca	97
	Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser	
	20 25 30	
5	gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat	145
	Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp	
	35 40 45	
10	ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct	193
	Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala	
	50 55 60	
15	cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg	241
	Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly	
	65 70 75 80	
20	ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa	289
	Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu	
	85 90 95	
25	gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc	337
	Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly	
	100 105 110	
30	cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg	385
	His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu	
	115 120 125	
35	gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg	433
	Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly	
	130 135 140	
40	cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc	481
	Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly	
	145 150 155 160	
45	atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga	529
	Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg	
	165 170 175	
50	gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca	577
	Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser	
	180 185 190	
55	tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc	625
	Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala	
	195 200 205	
60	aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc	673
	Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr	
	210 215 220	
65	aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa	721
	Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys	

- 107 -

	225		230		235		240	
	cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt							769
5	Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu	245		250		255		
	ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa							817
	Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln	260		265		270		
10	ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat							865
	Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp	275		280		285		
	gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat							913
15	Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn	290		295		300		
	aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat							961
20	Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His	305		310		315		320
	aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac							1009
25	Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp	325		330		335		
	ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa							1057
	Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys	340		345		350		
30	ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct							1105
	Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala	355		360		365		
	cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc							1153
35	Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu	370		375		380		
	cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga							1201
40	Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg	385		390		395		400
	tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt							1249
45	Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val	405		410		415		
	gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc							1297
	Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly	420		425		430		
50	aat atc act cct cat gct att gtc atc ttg cct aaa							1333
	Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys	435		440				

- 108 -

<210> 14
 <211> 444
 <212> PRT
 5 <213> Homo sapiens

<400> 14
 Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
 1 5 10 15
 10 Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser
 20 25 30
 15 Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
 35 40 45
 Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
 50 55 60
 20 Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
 65 70 75 80
 Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
 85 90 95
 25 Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
 100 105 110
 30 His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
 115 120 125
 Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
 130 135 140
 35 Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly
 145 150 155 160
 Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg
 165 170 175
 40 Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser
 180 185 190
 Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala
 195 200 205
 45 Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr
 210 215 220
 50 Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys
 225 230 235 240
 Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu
 245 250 255

- 109 -

Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln
 260 265 270

5 Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp
 275 280 285

Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn
 290 295 300

10 Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His
 305 310 315 320

15 Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
 325 330 335

Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
 340 345 350

20 Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
 355 360 365

Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
 370 375 380

25 Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
 385 390 395 400

30 Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
 405 410 415

Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
 420 425 430

35 Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
 435 440

40 <210> 15
 <211> 1332
 <212> DNA
 <213> Homo sapiens

45 <220>
 <221> CDS
 <222> (1)..(1332)

50 <400> 15
 acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac 48
 Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
 1 5 10 15

 cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca 96
 Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser

- 110 -

	20	25	30	
5	gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat Glu Ser Ser 35 Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp 45	40	45	144
10	ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala 50 55 60			192
15	cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly 65 70 75 80			240
20	ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu 85 90 95			288
25	gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly 100 105 110			336
30	cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu 115 120 125			384
35	gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly 130 135 140			432
40	cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly 145 150 155 160			480
45	atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg 165 170 175			528
50	gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser 180 185 190			576
55	tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala 195 200 205			624
60	aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr 210 215 220			672
65	aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys 225 230 235 240			720

- 111 -

	cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt	768
	Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu	
	245 250 255	
5	ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa	816
	Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln	
	260 265 270	
10	ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat	864
	Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp	
	275 280 285	
15	gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat	912
	Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn	
	290 295 300	
20	aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat	960
	Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His	
	305 310 315 320	
25	aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac	1008
	Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp	
	325 330 335	
30	ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa	1056
	Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys	
	340 345 350	
35	ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct	1104
	Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala	
	355 360 365	
40	cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc	1152
	Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu	
	370 375 380	
45	cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga	1200
	Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg	
	385 390 395 400	
50	tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt	1248
	Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val	
	405 410 415	
55	gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc	1296
	Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly	
	420 425 430	
60	aat atc act cct cat gct att gtc atc ttg cct aaa	1332
	Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys	
	435 440	